AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph on page 3, beginning at line 1 and ending at and including line 17, with the following rewritten paragraph.

--(i.e. gaps) as compared to the initial reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical amino acid residue occurs in both sequences to yield the number of match positions, dividing the number of match positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. When calculating the percentage sequence identity the sequences may be aligned allowing for up to 3 gaps with the *proviso* that in respect of the gaps, a total of not more than 15 amino acid residues is affected. Optimal alignment of sequences for comparison may also be conducted by computerised implementations of known algorithms. In a particular embodiment of the present invention the sequence identity is calculated using the FASTA version 3 algorithm which uses the method of Pearson and Lipman (Lipman, D.J. and Pearson, W.R. (1985) Rapid and sensitive protein similarity searches, ~~and Science.~~ Science 227:1435-1441 and Pearson, W.R. and Lipman, D.J. (1988) Improved tools for biological sequence ~~comparison~~analysis. PNAS[.] 85:2444-2448) to search for similarities between the reference sequence (also termed the query sequence) and any group of sequences (termed further sequences). Methods also exist in the art which enable the percentage sequence identity between polynucleotide sequences to be calculated.--